

FIG. 1

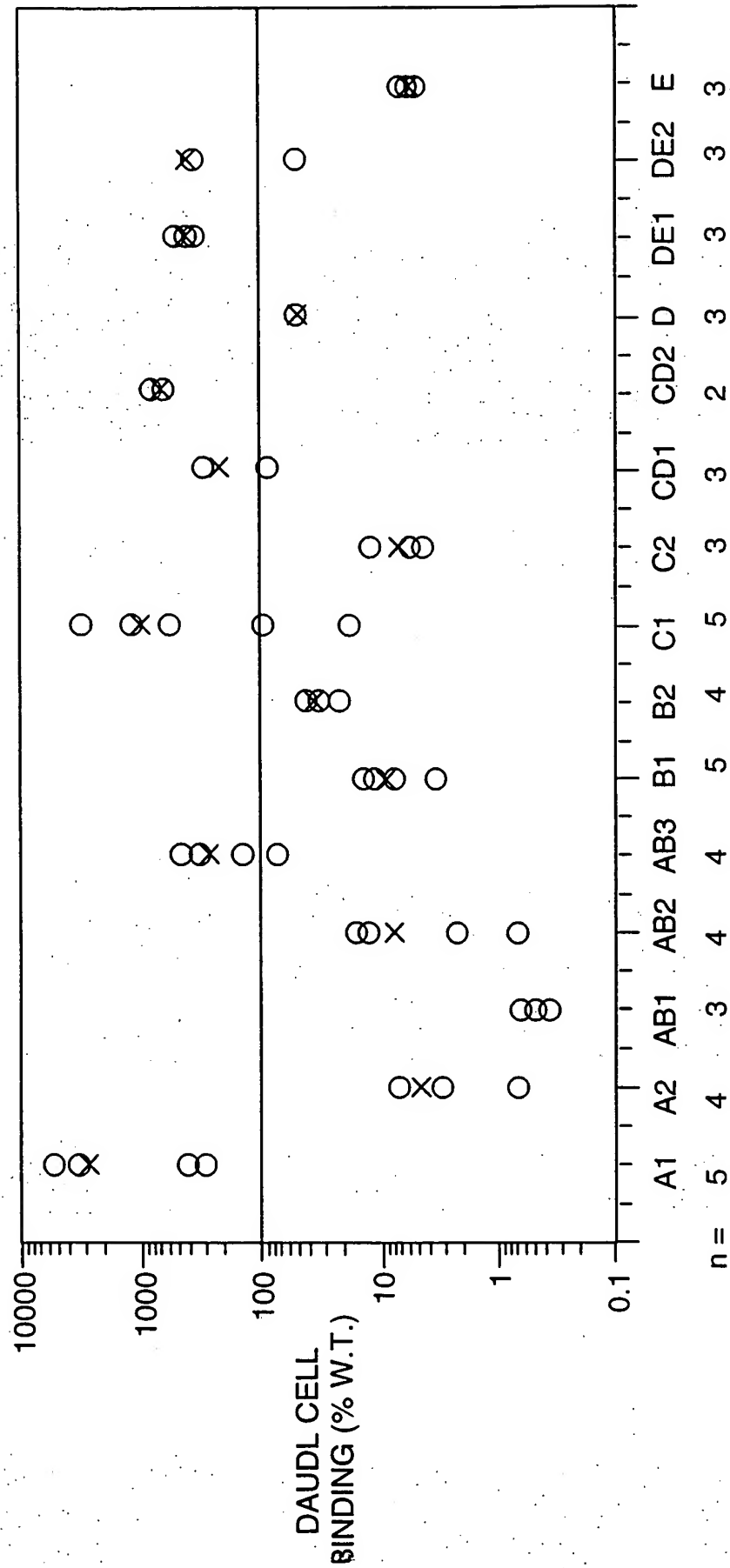


FIG. 2



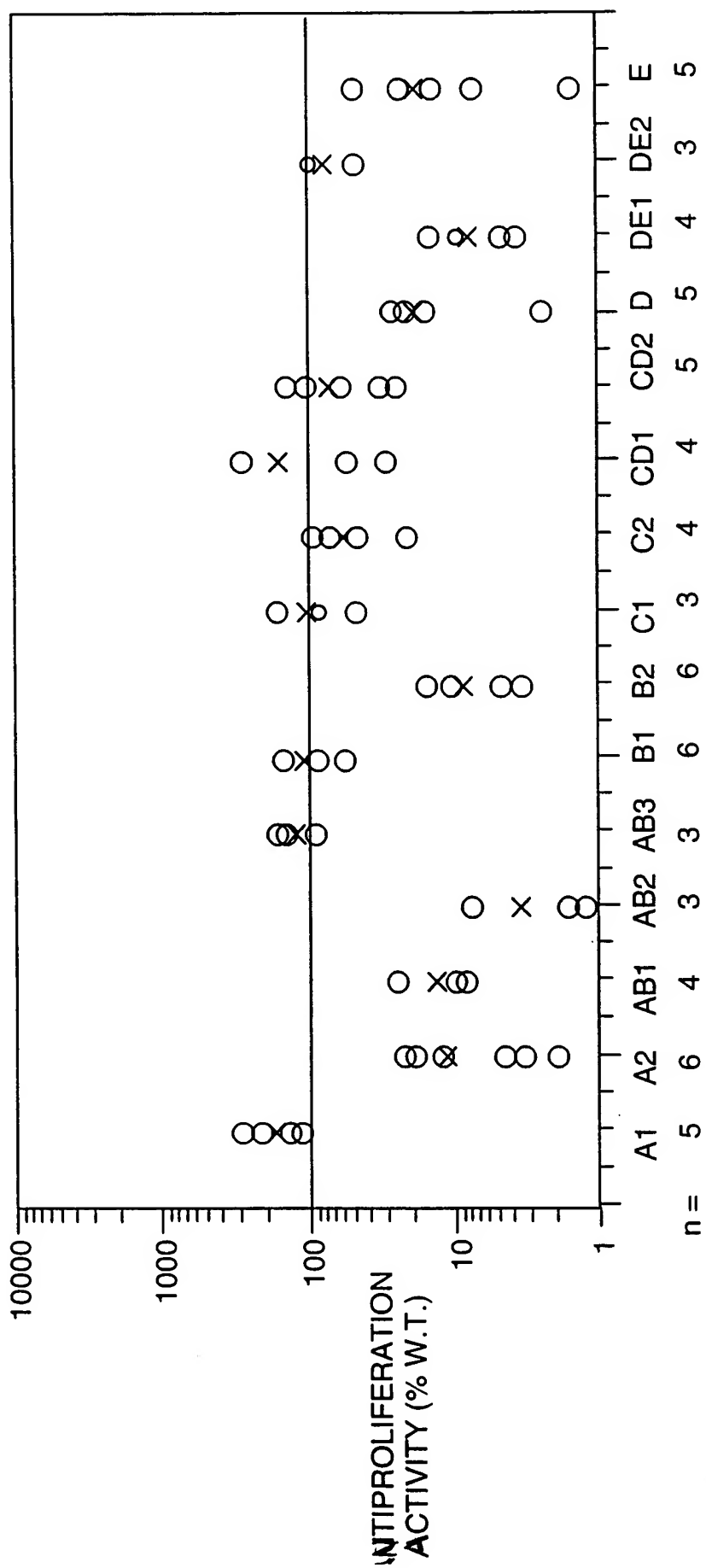
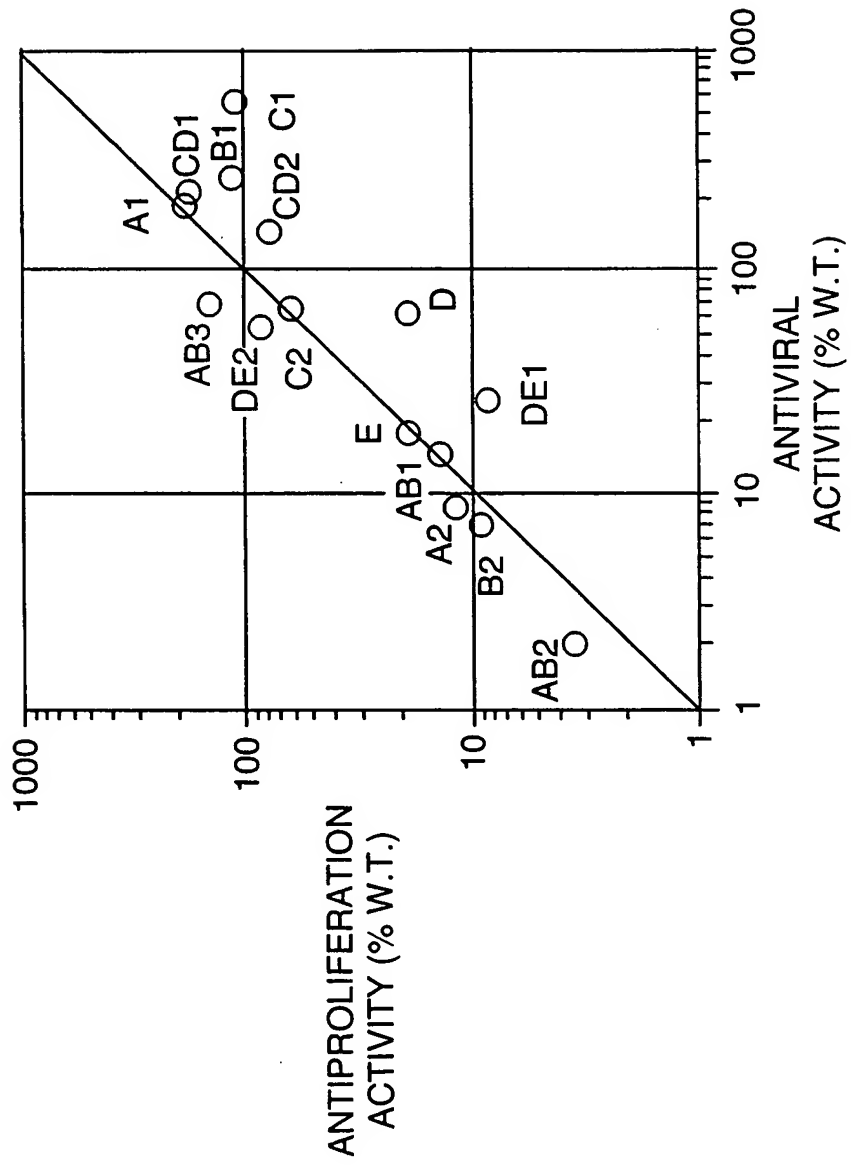


FIG. 4



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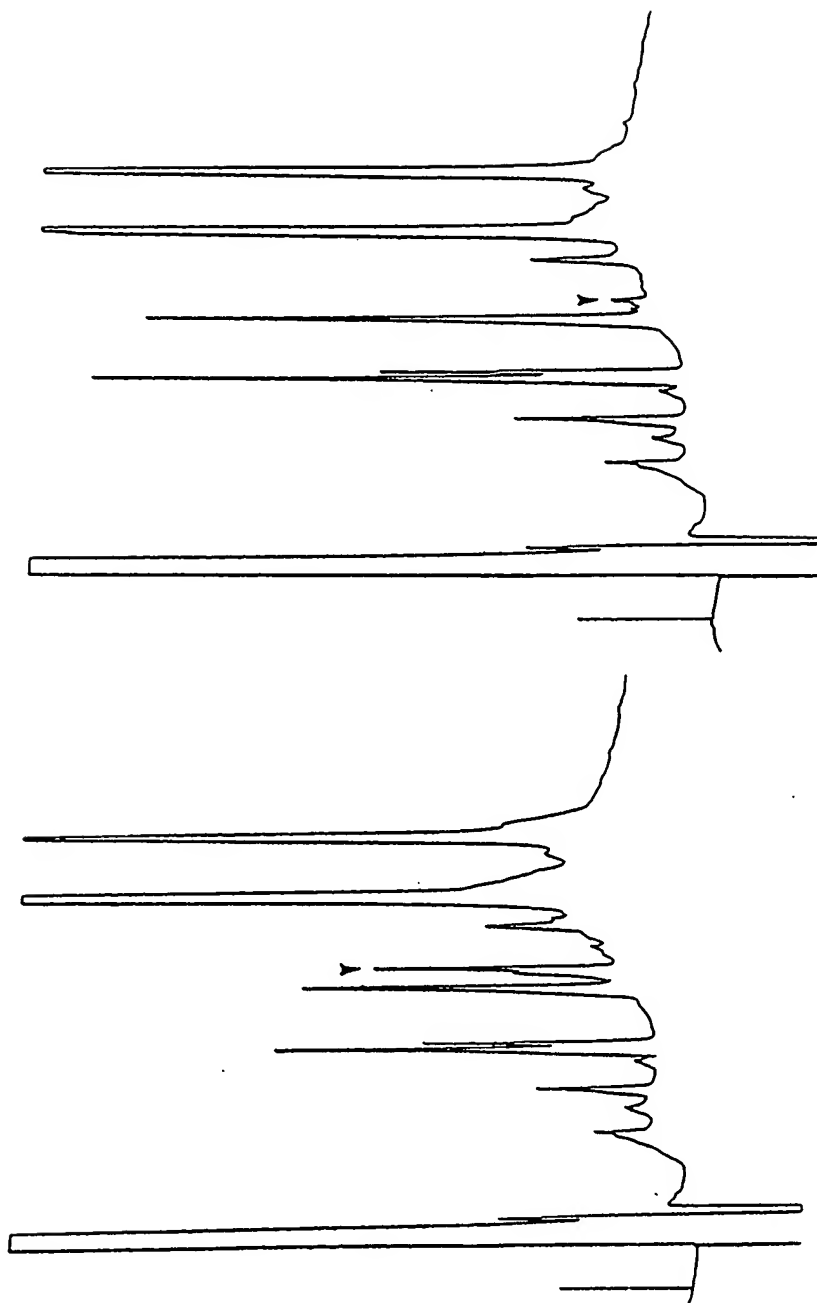


FIG. 6B

FIG. 6A

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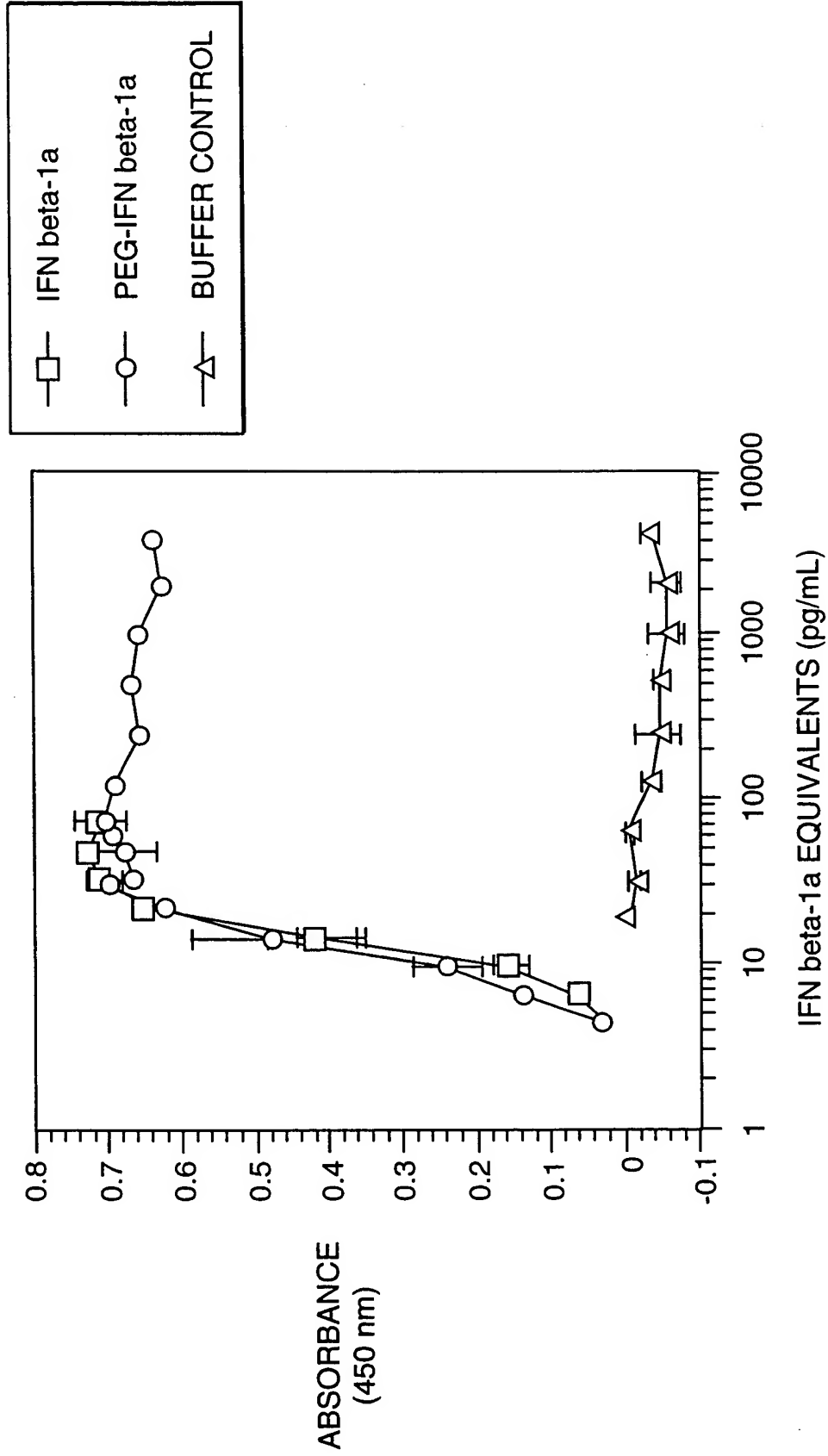


FIG. 7

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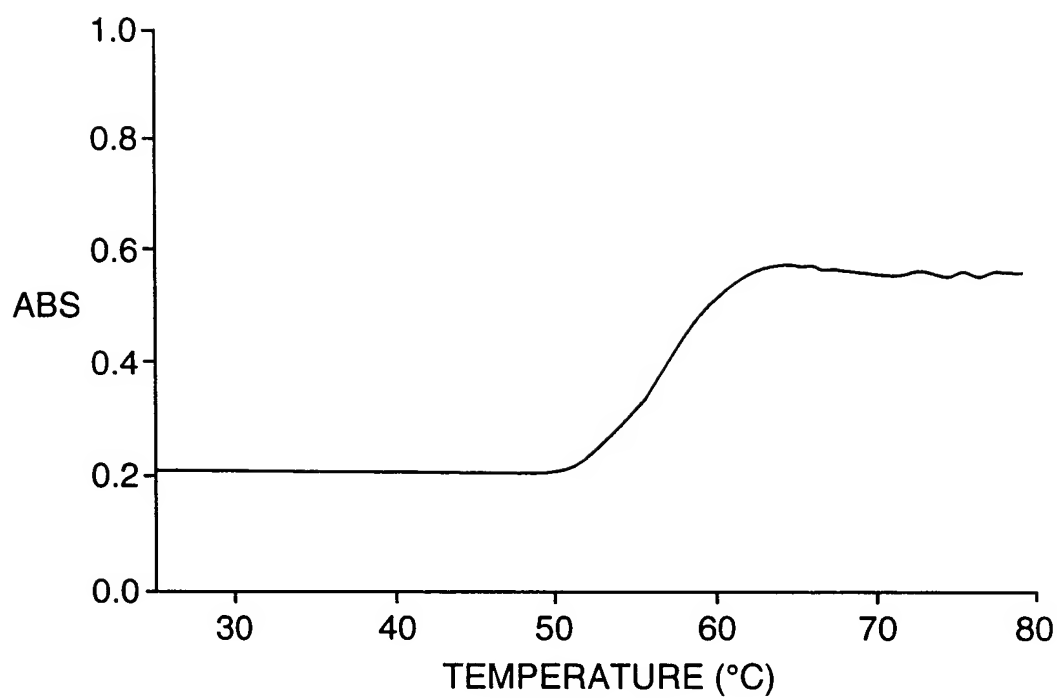


FIG. 8a

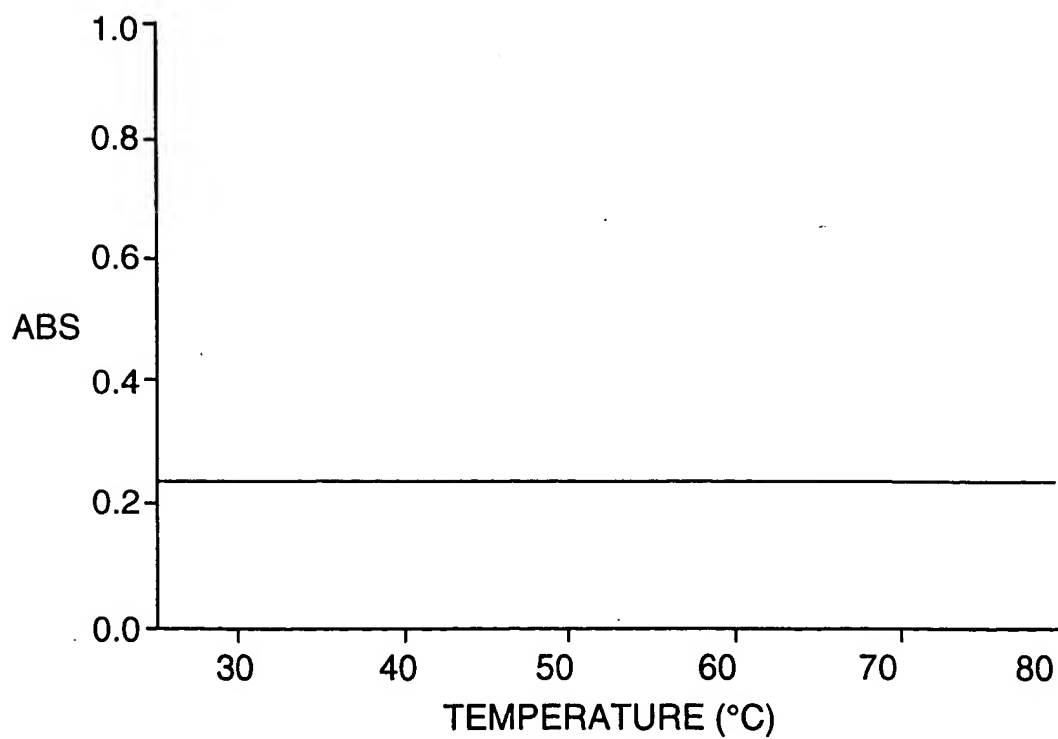


FIG. 8b



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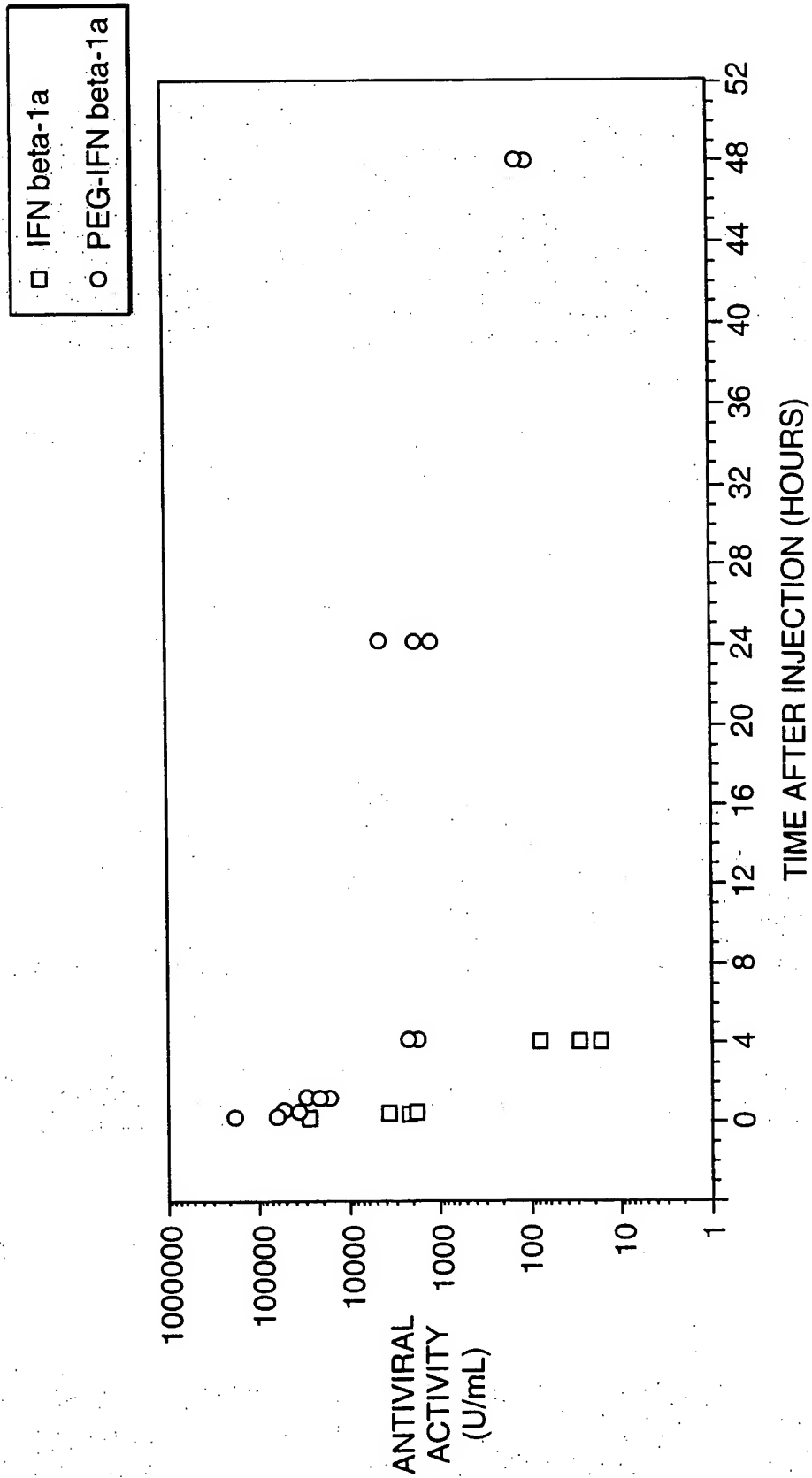


FIG. 9

1 TCCGGGGGCC ATCATCATCA TCATCATAGC TCCGGAGACG ATGATGACAA GATGAGCTAC  
 AGGCCCCCGG TAGTAGTAGT AGTAGTATCG AGGCCTCTGC TACTACTGTT CTACTIONGATG  
 1 ▶ Ser Gly Gly His His His His His Ser Ser Gly Asp Asp Asp Lys Met Ser Tyr  
 61 AACTTGCTTG GATTCTACA AAGAAGCAGC AATTTTCAGT GTCAGAAGCT CCTGTGGCAA  
 TTGAACGAAC CTAAGGATGT TTCTTCGTCG TTAAGAGTCA CAGTCTTCGA GGACACCGTT  
 21 ▶ Asn Leu Leu Gly Phe Leu Glu Arg Ser Ser Asn Phe Glu Asn Lys Leu Leu Trp Glu  
 121 TTGAATGGGA GGCTTGAATA CTGCCTCAAG GACAGGATGA ACTTTGACAT CCCTGAGGAG  
 AACTTACCCT CCGAAGTTAT GACGGAGTTC CTGTCCTACT TGAAACTGTA GGGACTCCTC  
 41 ▶ Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asn Ile Pro Glu Glu  
 181 ATTAAGCAGC TGCAGCAGTT CCAGAAGGAG GACGCCGCAT TGACCATCTA TGAGATGCTC  
 TAATTCGTCG ACGTCGTCAG GGTCTTCCTC CTGCGGCGTA ACTGGTAGAT ACTCTACGAG  
 61 ▶ Ile Lys Glu Leu Glu Glu Phe Glu Lys Glu Asp Ala Ala Leu Thr Ile Tyr Arg Met Leu  
 241 CAGAACATCT TTGCTATTTT CAGACAAGAT TCATCTAGCA CTGGCTGGAA TGAGACTATT  
 GTCTTGATGA AACGATAAAA GTCTGTTCTA AGTAGATCGT GACCGACCTT ACTCTGATAA  
 81 ▶ Glu Asn Ile Phe Ala Ile Phe Arg Glu Asn Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile  
 301 GTTGAGAACC TCCTGGCTAA TGTCTATCAT CAGATAAACC ATCTGAAGAC AGTCCTGGAA  
 CAACTCTTGG AGGACCGATT ACAGATAGTA GTCTATTTGG TAGACTTCTG TCAGGACCTT  
 101 ▶ Val Glu Asn Leu Leu Ala Asn Val Tyr His Glu Ile Asn His Leu Lys Thr Val Leu Glu  
 361 GAAAAACTGG AGAAAGAAGA TTTCACCAGG GGAAAACTCA TGAGCAGTCT GCACCTGAAA  
 CTTTTTGACC TCTTTCTTCT AAAGTGGTCC CTTTTGAGT ACTCGTCAGA CGTGGACTTT  
 121 ▶ Glu Lys Leu Glu Lys Glu Asn Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys  
 421 AGATATTATG GGAGGATTCT GCATTACCTG AAGGCCAAGG AGTACAGTCA CTGTGCCTGG  
 TCTATAATAC CCTCCTAAGA CGTAATGGAC TTCCGGTTCC TCATGTCAGT GACACGGACC  
 141 ▶ Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp  
 481 ACCATAGTCA GAGTGGAAAT CCTAAGGAAC TTTTACTTCA TTAACAGACT TACAGGTTAC  
 TGGTATCAGT CTCACCTTTA GGATTCCTTG AAAATGAAGT AATTGTCTGA ATGTCCAATG  
 161 ▶ Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr  
 541 CTCCGAAAC  
 GAGGCTTTG  
 181 ▶ Leu Arg Asn

FIG. 10

